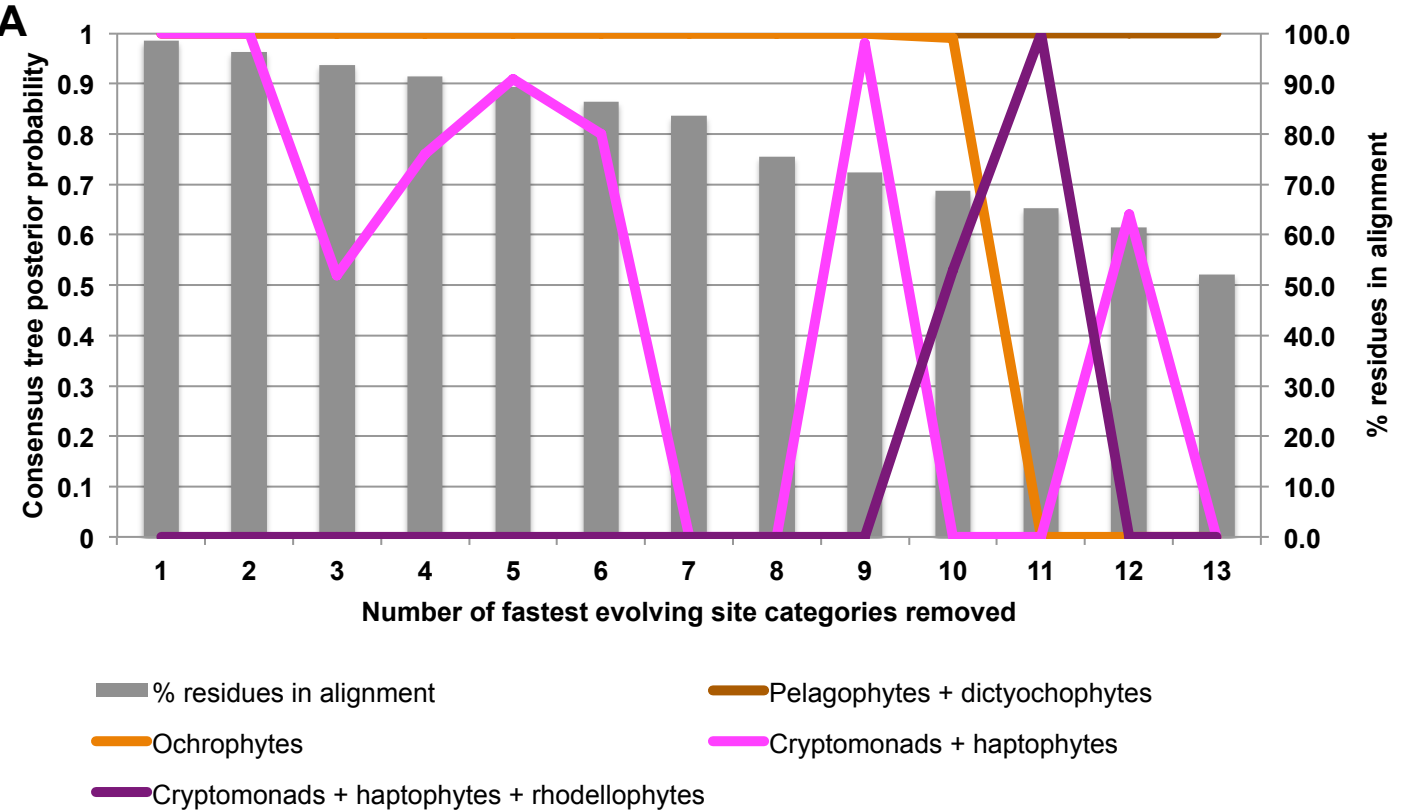


**Fig. 9- figure supplement 2. Fast site removal and clade deduction analysis of plastid genome trees. Panel A** shows the support values obtained for Bayesian + Jones trees inferred from modified versions of the taxon-rich plastid multigene alignment from which the 13 fastest-evolving site categories had been removed for four different branching relationships pertaining to the placements of haptophyte and hypogyristean sequences. The % of residues from the original alignment retained in each modified alignment are shown with grey bars. **Panel B** tabulates the support obtained for two different evolutionary relationships (haptophytes as a sister group to all cryptomonads, and as a sister group to all ochrophytes) in gene-rich (i) and taxon-rich (ii) alignments modified to remove all amino acids that occur at different frequencies in haptophytes to ochrophyte lineages, and modified to remove individual or pairs of CASH lineages. “x” indicates that the topology in question was not obtained.



**B**

Topology	Tree	No glycines	No variant aa	No diatoms	No chrysista	No cryptomonads	No diatoms + chrysista	No diatoms + cryptomonads	No chrysista + cryptomonads
i) Gene-rich alignment									
cryptomonads + haptophytes	MrBayes	1	1	1	1	x	x	x	x
cryptomonads + haptophytes	RAXML	95	97	98	62	x	30	x	x
haptophytes + ochrophytes	MrBayes	x	x	x	x	1	x	1	1
haptophytes + ochrophytes	RAXML	x	x	x	x	100	x	100	100
ii) Taxon-rich alignment									
cryptomonads + haptophytes	MrBayes	1	0.84	1	1	x	x	x	x
cryptomonads + haptophytes	RAXML	35	x	x	x	x	x	x	x
haptophytes + ochrophytes	MrBayes	x	x	x	x	1	1	1	1
haptophytes + ochrophytes	RAXML	x	x	43	73	100	69	100	100